10091281

Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term:

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search Clear Interrupt

Search History

DATE: Wednesday, April 14, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L2	optineurin and hybridiz$5	2	L2
L1	optineurin and (polymerase chain reaction or PCR)	0	L1

END OF SEARCH HISTORY

Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: 13 and prognos$3

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

Search Clear Interrupt

Search History

DATE: Wednesday, April 14, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L6	l3 and prognos$3	12	L6
DB=EPAB; PLUR=YES; OP=ADJ			
L5	WO-200042220-A1.did.	0	L5
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L4	L3 and optineurin	1	L4
L3	L2 and (detect$3 near5 polymorphism$1)	22	L3
L2	glaucoma same (hybridiz$5 or polymerase chain reaction or PCR)	124	L2
L1	glaucoma and (hybridiz$5 or polymerase chain reaction or PCR)	779	L1

END OF SEARCH HISTORY

10091281

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FILE 'HOME' ENTERED AT 11:10:28 ON 14 APR 2004

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COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

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FILE 'EMBASE' ENTERED AT 11:10:47 ON 14 APR 2004
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=> s (iagnos### or detect### or prognos###)(P)optineurin
L1          28 (IAGNOS### OR DETECT### OR PROGNOS###)(P) OPTINEURIN

=> s l1 and hybridiz#####
L2           2 L1 AND HYBRIDIZ#####

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3           2 DUP REM L2 (0 DUPLICATES REMOVED)

=> d l3 1-2 bib ab kwic

L3   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2004:117279  CAPLUS
DN   140:176202
TI   Gene assay method for predicting glaucoma onset risk using human
     optineurin gene-specific primers for detecting mutations
IN   Kouchi, Yasuhiro; Masago, Akinori; Takahata, Takayuki
PA   Sysmex Corporation, Japan
SO   Eur. Pat. Appl., 31 pp.
     CODEN: EPXXDW
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     --------------    ----  --------       ---------------  --------
PI   EP 1388590         A2   20040211       EP 2003-447201   20030729
        R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
            IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
PRAI JP 2002-226612     A    20020802
AB   Future onset of glaucoma is predicted using as a marker, mutation of
     base(s) in a coding region of a glaucoma-related gene encoding optineurin
     (OPTN gene).  The OPTN gene-specific oligonucleotide primers and the
     nucleotide sequence of the coding region of human OPTN gene are provided.
TI   Gene assay method for predicting glaucoma onset risk using human
     optineurin gene-specific primers for detecting mutations
IT   Gene, animal
     RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
     use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
     USES (Uses)
        (OPTN; gene assay method for predicting glaucoma onset risk using human
        optineurin gene-specific primers for detecting
        mutations)
IT   Mutation
```

(deletion; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(exon; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Genetic polymorphism
Glaucoma (disease)
Human
Mutation
Nucleic acid amplification (method)
Nucleic acid **hybridization**
PCR (polymerase chain reaction)
Risk assessment
Susceptibility (genetic)
Test kits
(gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Mutation
(insertion; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT DNA sequences
(of OPTN gene; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Glaucoma (disease)
(open-angle glaucoma; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**optineurin**; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT Mutation
(substitution; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT 657708-60-6, DNA (human gene OPTN coding region)
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT 657708-61-7 657708-62-8 657708-63-9 657708-64-0 657708-65-1
657708-66-2 657708-67-3 657708-68-4 657708-69-5 657708-70-8
657708-71-9 657708-72-0 657708-73-1 657708-74-2 657708-75-3
657708-76-4 657708-77-5 657708-78-6 657708-79-7 657708-80-0
657708-81-1 657708-82-2 657708-83-3 657708-84-4 657708-85-5
657708-86-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical

study); BIOL (Biological study); USES (Uses)
(primer; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

IT 657709-19-8, 2: PN: EP1388590 SEQID: 2 unclaimed DNA 657709-20-1, 3: PN: EP1388590 SEQID: 3 unclaimed DNA 657709-21-2, 4: PN: EP1388590 SEQID: 4 unclaimed DNA 657709-22-3, 5: PN: EP1388590 SEQID: 5 unclaimed DNA 657709-23-4, 6: PN: EP1388590 SEQID: 6 unclaimed DNA 657709-24-5, 7: PN: EP1388590 SEQID: 7 unclaimed DNA 657709-25-6, 8: PN: EP1388590 SEQID: 8 unclaimed DNA 657709-26-7, 9: PN: EP1388590 SEQID: 9 unclaimed DNA 657709-27-8 657709-28-9 657709-29-0 657709-30-3 657709-31-4
RL: PRP (Properties)
(unclaimed nucleotide sequence; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for **detecting** mutations)

L3 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:796207 CAPLUS
DN 139:303000
TI Promoter sequences of human optineurin gene and uses in diagnosis of glaucoma
IN Raymond, Vincent; Morissette, Jean; Si, Erwin
PA Can.
SO U.S. Pat. Appl. Publ., 159 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003190617	A1	20031009	US 2002-91281	20020306
PRAI	US 2002-91281		20020306		

AB Promoter sequences of the human **optineurin** gene can be used to diagnose, **prognoses**, and treat glaucoma and related disorders. Methods, kits, and nucleic acids capable of **detecting** or containing polymorphisms located within the promoter region of the **optineurin** gene are also provided. The promoter sequences can also be used to generate cells, vectors, and nucleic acids useful in a variety of diagnostic and **prognostic** methods and kits as well as therapeutic compds., compns. and methods.
AB Promoter sequences of the human **optineurin** gene can be used to diagnose, **prognoses**, and treat glaucoma and related disorders. Methods, kits, and nucleic acids capable of **detecting** or containing polymorphisms located within the promoter region of the **optineurin** gene are also provided. The promoter sequences can also be used to generate cells, vectors, and nucleic acids useful in a variety of diagnostic and **prognostic** methods and kits as well as therapeutic compds., compns. and methods.

IT Blood
Blood serum
Body fluid
DNA sequences
Eye, disease
Genetic markers
Glaucoma (disease)
Human
Lymph
Molecular cloning
Nucleic acid amplification (method)
Nucleic acid **hybridization**
PCR (polymerase chain reaction)
Susceptibility (genetic)
(promoter sequences of human optineurin gene and uses in diagnosis of glaucoma)

```
=> s Raymond.in.
L4        1308 RAYMOND.IN.

=> s l4 and optineurin
L5           0 L4 AND OPTINEURIN

=> s morissette.in.
L6           2 MORISSETTE.IN.

=> s l6 and optineurin
L7           0 L6 AND OPTINEURIN

=> s si.in.
L8      926052 SI.IN.

=> s l8 and optineurin
L9           0 L8 AND OPTINEURIN

=> s optineuin gene and hybridiz#####
L10          0 OPTINEUIN GENE AND HYBRIDIZ#####

=> s optineurin gene and hybridiz#####
L11          2 OPTINEURIN GENE AND HYBRIDIZ#####

=> d l11 1-2 bib ab kwic

L11  ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2004:117279  CAPLUS
DN   140:176202
TI   Gene assay method for predicting glaucoma onset risk using human
     optineurin gene-specific primers for detecting mutations
IN   Kouchi, Yasuhiro; Masago, Akinori; Takahata, Takayuki
PA   Sysmex Corporation, Japan
SO   Eur. Pat. Appl., 31 pp.
     CODEN: EPXXDW
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   EP 1388590         A2   20040211       EP 2003-447201   20030729
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
PRAI JP 2002-226612     A    20020802
AB   Future onset of glaucoma is predicted using as a marker, mutation of
     base(s) in a coding region of a glaucoma-related gene encoding optineurin
     (OPTN gene).  The OPTN gene-specific oligonucleotide primers and the
     nucleotide sequence of the coding region of human OPTN gene are provided.
TI   Gene assay method for predicting glaucoma onset risk using human
     optineurin gene-specific primers for detecting mutations
ST   optineurin gene sequence mutation primer glaucoma risk
     human
IT   Gene, animal
     RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
     use); PRP (Properties); ANST (Analytical study); BIOL (Biological study);
     USES (Uses)
        (OPTN; gene assay method for predicting glaucoma onset risk using human
        optineurin gene-specific primers for detecting
        mutations)
IT   Mutation
        (deletion; gene assay method for predicting glaucoma onset risk using
        human optineurin gene-specific primers for
```

detecting mutations)
IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(exon; gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT Genetic polymorphism
Glaucoma (disease)
Human
Mutation
Nucleic acid amplification (method)
Nucleic acid **hybridization**
PCR (polymerase chain reaction)
Risk assessment
Susceptibility (genetic)
Test kits
(gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT Mutation
(insertion; gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT DNA sequences
(of OPTN gene; gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT Glaucoma (disease)
(open-angle glaucoma; gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**optineurin**; **gene** assay method for predicting glaucoma onset risk using human **optineurin gene** -specific primers for detecting mutations)
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(substitution; gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
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RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; gene assay method for predicting glaucoma onset risk using human **optineurin gene**-specific primers for detecting mutations)
IT 657708-61-7 657708-62-8 657708-63-9 657708-64-0 657708-65-1
657708-66-2 657708-67-3 657708-68-4 657708-69-5 657708-70-8
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657708-76-4 657708-77-5 657708-78-6 657708-79-7 657708-80-0
657708-81-1 657708-82-2 657708-83-3 657708-84-4 657708-85-5
657708-86-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; gene assay method for predicting glaucoma onset risk using

human **optineurin gene**-specific primers for detecting mutations)

IT 657709-19-8, 2: PN: EP1388590 SEQID: 2 unclaimed DNA 657709-20-1, 3: PN: EP1388590 SEQID: 3 unclaimed DNA 657709-21-2, 4: PN: EP1388590 SEQID: 4 unclaimed DNA 657709-22-3, 5: PN: EP1388590 SEQID: 5 unclaimed DNA 657709-23-4, 6: PN: EP1388590 SEQID: 6 unclaimed DNA 657709-24-5, 7: PN: EP1388590 SEQID: 7 unclaimed DNA 657709-25-6, 8: PN: EP1388590 SEQID: 8 unclaimed DNA 657709-26-7, 9: PN: EP1388590 SEQID: 9 unclaimed DNA 657709-27-8 657709-28-9 657709-29-0 657709-30-3 657709-31-4
RL: PRP (Properties)
(unclaimed nucleotide sequence; gene assay method for predicting glaucoma onset risk using human **optineurin gene** -specific primers for detecting mutations)

L11 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:796207 CAPLUS
DN 139:303000
TI Promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma
IN Raymond, Vincent; Morissette, Jean; Si, Erwin
PA Can.
SO U.S. Pat. Appl. Publ., 159 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003190617	A1	20031009	US 2002-91281	20020306
PRAI	US 2002-91281		20020306		

AB Promoter sequences of the human **optineurin gene** can be used to diagnose, prognoses, and treat glaucoma and related disorders. Methods, kits, and nucleic acids capable of detecting or containing polymorphisms located within the promoter region of the **optineurin gene** are also provided. The promoter sequences can also be used to generate cells, vectors, and nucleic acids useful in a variety of diagnostic and prognostic methods and kits as well as therapeutic compds., compns. and methods.
TI Promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma
AB Promoter sequences of the human **optineurin gene** can be used to diagnose, prognoses, and treat glaucoma and related disorders. Methods, kits, and nucleic acids capable of detecting or containing polymorphisms located within the promoter region of the **optineurin gene** are also provided. The promoter sequences can also be used to generate cells, vectors, and nucleic acids useful in a variety of diagnostic and prognostic methods and kits as well as therapeutic compds., compns. and methods.
ST promoter sequence **optineurin gene** human diagnosis glaucoma
IT Bacteria (Eubacteria)
Eye
(as expression host; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Test kits
(diagnostic; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(for optineurin; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Diagnosis
(genetic; promoter sequences of human **optineurin gene**

and uses in diagnosis of glaucoma)
IT Proteins
RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(green fluorescent, as reporter; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Animal cell
(mammalian, as expression host; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Diagnosis
(mol.; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Nerve
(optic; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(optineurin; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Blood
Blood serum
Body fluid
DNA sequences
Eye, disease
Genetic markers
Glaucoma (disease)
Human
Lymph
Molecular cloning
Nucleic acid amplification (method)
Nucleic acid **hybridization**
PCR (polymerase chain reaction)
Susceptibility (genetic)
(promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Antisense RNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Primers (nucleic acid)
Promoter (genetic element)
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Eye
(retina; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Genetic polymorphism
(single nucleotide; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT Eye
(trabecular meshwork; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT 9014-00-0, Luciferase
RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(as reporter; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)
IT 611241-00-0 611245-15-9 611245-16-0 611245-17-1
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)

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611243-05-1 611243-06-2 611243-07-3 611243-08-4 611243-09-5
611243-10-8
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(**optineurin gene** fragment sequence; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)

IT 611243-11-9 611243-12-0 611243-13-1 611243-14-2 611243-15-3
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611245-11-5 611245-12-6 611245-13-7 611245-14-8
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(**optineurin gene** fragment sequence; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)

IT 65-71-4, Thymine 71-30-7, Cytosine 73-24-5, Adenine, analysis 73-40-5, Guanine
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)

IT 611251-44-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; promoter sequences of human **optineurin gene** and uses in diagnosis of glaucoma)

=> s optineurin and hybridiz#####
L12 2 OPTINEURIN AND HYBRIDIZ#####

=> d l12 1-2 bib ab

L12 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:117279 CAPLUS
DN 140:176202
TI Gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations
IN Kouchi, Yasuhiro; Masago, Akinori; Takahata, Takayuki
PA Sysmex Corporation, Japan
SO Eur. Pat. Appl., 31 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE

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PI   EP 1388590        A2   20040211       EP 2003-447201   20030729
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
PRAI JP 2002-226612    A    20020802
AB   Future onset of glaucoma is predicted using as a marker, mutation of
     base(s) in a coding region of a glaucoma-related gene encoding
     optineurin (OPTN gene). The OPTN gene-specific oligonucleotide
     primers and the nucleotide sequence of the coding region of human OPTN
     gene are provided.

L12  ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2003:796207  CAPLUS
DN   139:303000
TI   Promoter sequences of human optineurin gene and uses in
     diagnosis of glaucoma
IN   Raymond, Vincent; Morissette, Jean; Si, Erwin
PA   Can.
SO   U.S. Pat. Appl. Publ., 159 pp.
     CODEN: USXXCO
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   US 2003190617      A1   20031009       US 2002-91281    20020306
PRAI US 2002-91281           20020306
AB   Promoter sequences of the human optineurin gene can be used to
     diagnose, prognoses, and treat glaucoma and related disorders. Methods,
     kits, and nucleic acids capable of detecting or containing polymorphisms
     located within the promoter region of the optineurin gene are
     also provided. The promoter sequences can also be used to generate cells,
     vectors, and nucleic acids useful in a variety of diagnostic and
     prognostic methods and kits as well as therapeutic compds., compns. and
     methods.


=> s optineurin and(polymerase chain reaction or PCR)
L13          26 OPTINEURIN AND(POLYMERASE CHAIN REACTION OR PCR)

=> dup rem l13
PROCESSING COMPLETED FOR L13
L14           15 DUP REM L13 (11 DUPLICATES REMOVED)

=> d l14 1-15 bib ab kwic

L14  ANSWER 1 OF 15  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2004:117279  CAPLUS
DN   140:176202
TI   Gene assay method for predicting glaucoma onset risk using human
     optineurin gene-specific primers for detecting mutations
IN   Kouchi, Yasuhiro; Masago, Akinori; Takahata, Takayuki
PA   Sysmex Corporation, Japan
SO   Eur. Pat. Appl., 31 pp.
     CODEN: EPXXDW
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   EP 1388590        A2   20040211       EP 2003-447201   20030729
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
PRAI JP 2002-226612    A    20020802
```

AB Future onset of glaucoma is predicted using as a marker, mutation of base(s) in a coding region of a glaucoma-related gene encoding **optineurin** (OPTN gene). The OPTN gene-specific oligonucleotide primers and the nucleotide sequence of the coding region of human OPTN gene are provided.

TI Gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations

AB Future onset of glaucoma is predicted using as a marker, mutation of base(s) in a coding region of a glaucoma-related gene encoding **optineurin** (OPTN gene). The OPTN gene-specific oligonucleotide primers and the nucleotide sequence of the coding region of human OPTN gene are provided.

ST **optineurin** gene sequence mutation primer glaucoma risk human

IT Gene, animal
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(OPTN; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Mutation
(deletion; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Genetic element
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(exon; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Genetic polymorphism
Glaucoma (disease)
Human
Mutation
Nucleic acid amplification (method)
Nucleic acid hybridization
PCR (polymerase chain reaction)
Risk assessment
Susceptibility (genetic)
Test kits
(gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Mutation
(insertion; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT DNA sequences
(of OPTN gene; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Glaucoma (disease)
(open-angle glaucoma; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**optineurin**; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT Mutation

(substitution; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT 657708-60-6, DNA (human gene OPTN coding region)
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT 657708-61-7 657708-62-8 657708-63-9 657708-64-0 657708-65-1
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657708-71-9 657708-72-0 657708-73-1 657708-74-2 657708-75-3
657708-76-4 657708-77-5 657708-78-6 657708-79-7 657708-80-0
657708-81-1 657708-82-2 657708-83-3 657708-84-4 657708-85-5
657708-86-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

IT 657709-19-8, 2: PN: EP1388590 SEQID: 2 unclaimed DNA 657709-20-1, 3: PN: EP1388590 SEQID: 3 unclaimed DNA 657709-21-2, 4: PN: EP1388590 SEQID: 4 unclaimed DNA 657709-22-3, 5: PN: EP1388590 SEQID: 5 unclaimed DNA 657709-23-4, 6: PN: EP1388590 SEQID: 6 unclaimed DNA 657709-24-5, 7: PN: EP1388590 SEQID: 7 unclaimed DNA 657709-25-6, 8: PN: EP1388590 SEQID: 8 unclaimed DNA 657709-26-7, 9: PN: EP1388590 SEQID: 9 unclaimed DNA 657709-27-8 657709-28-9 657709-29-0 657709-30-3 657709-31-4
RL: PRP (Properties)
(unclaimed nucleotide sequence; gene assay method for predicting glaucoma onset risk using human **optineurin** gene-specific primers for detecting mutations)

L14 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:796207 CAPLUS
DN 139:303000
TI Promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma
IN Raymond, Vincent; Morissette, Jean; Si, Erwin
PA Can.
SO U.S. Pat. Appl. Publ., 159 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003190617	A1	20031009	US 2002-91281	20020306
PRAI	US 2002-91281		20020306		

AB Promoter sequences of the human **optineurin** gene can be used to diagnose, prognoses, and treat glaucoma and related disorders. Methods, kits, and nucleic acids capable of detecting or containing polymorphisms located within the promoter region of the **optineurin** gene are also provided. The promoter sequences can also be used to generate cells, vectors, and nucleic acids useful in a variety of diagnostic and prognostic methods and kits as well as therapeutic compds., compns. and methods.

TI Promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma
AB Promoter sequences of the human **optineurin** gene can be used to diagnose, prognoses, and treat glaucoma and related disorders. Methods, kits, and nucleic acids capable of detecting or containing polymorphisms located within the promoter region of the **optineurin** gene are also provided. The promoter sequences can also be used to generate cells,

vectors, and nucleic acids useful in a variety of diagnostic and prognostic methods and kits as well as therapeutic compds., compns. and methods.

ST promoter sequence **optineurin** gene human diagnosis glaucoma

IT Bacteria (Eubacteria)
Eye
(as expression host; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Test kits
(diagnostic; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(for **optineurin**; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Diagnosis
(genetic; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Proteins
RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(green fluorescent, as reporter; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Animal cell
(mammalian, as expression host; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Diagnosis
(mol.; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Nerve
(optic; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**optineurin**; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Blood
Blood serum
Body fluid
DNA sequences
Eye, disease
Genetic markers
Glaucoma (disease)
Human
Lymph
Molecular cloning
Nucleic acid amplification (method)
Nucleic acid hybridization
PCR (polymerase chain reaction)
Susceptibility (genetic)
(promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Antisense RNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Primers (nucleic acid)
Promoter (genetic element)
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Eye

(retina; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Genetic polymorphism
(single nucleotide; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT Eye
(trabecular meshwork; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT 9014-00-0, Luciferase
RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(as reporter; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT 611241-00-0 611245-15-9 611245-16-0 611245-17-1
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT 141541-10-8 143519-57-7 184875-66-9 226385-52-0 247141-98-6
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611243-10-8
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(**optineurin** gene fragment sequence; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT 611243-11-9 611243-12-0 611243-13-1 611243-14-2 611243-15-3
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611244-31-6 611244-32-7 611244-33-8 611244-34-9 611244-35-0
611244-36-1 611244-37-2 611244-38-3 611244-39-4 611244-40-7
611244-41-8 611244-42-9 611244-43-0 611244-44-1 611244-45-2
611244-46-3 611244-47-4 611244-48-5 611244-49-6 611244-50-9
611244-51-0 611244-52-1 611244-53-2 611244-54-3 611244-55-4
611244-56-5 611244-57-6 611244-58-7 611244-59-8 611244-60-1
611244-61-2 611244-62-3 611244-63-4 611244-64-5 611244-65-6
611244-66-7 611244-67-8 611244-68-9 611244-69-0 611244-70-3
611244-71-4 611244-72-5 611244-73-6 611244-74-7 611244-75-8
611244-76-9 611244-77-0 611244-78-1 611244-79-2 611244-80-5
611244-81-6 611244-82-7 611244-83-8 611244-84-9 611244-85-0
611244-86-1 611244-87-2 611244-88-3 611244-89-4 611244-90-7
611244-91-8 611244-92-9 611244-93-0 611244-94-1 611244-95-2
611244-96-3 611244-97-4 611244-98-5 611244-99-6 611245-00-2
611245-01-3 611245-02-4 611245-03-5 611245-04-6 611245-05-7
611245-06-8 611245-07-9 611245-08-0 611245-09-1 611245-10-4
611245-11-5 611245-12-6 611245-13-7 611245-14-8
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(**optineurin** gene fragment sequence; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT 65-71-4, Thymine 71-30-7, Cytosine 73-24-5, Adenine, analysis
73-40-5, Guanine
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

IT 611251-44-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; promoter sequences of human **optineurin** gene and uses in diagnosis of glaucoma)

L14 ANSWER 3 OF 15 MEDLINE on STN DUPLICATE 1
AN 2003400828 MEDLINE
DN PubMed ID: 12939304

TI Different **optineurin** mutation pattern in primary open-angle glaucoma.
AU Leung Yuk Fai; Fan Bao Jian; Lam Dennis S C; Lee Wing Shan; Tam Pancy O S; Chua John K H; Tham Clement C Y; Lai Jimmy S M; Fan Dorothy S P; Pang Chi Pui
CS Department of Ophthalmology and Visual Sciences, the Chinese University of Hong Kong, Hong Kong, China.
SO Investigative ophthalmology & visual science, (2003 Sep) 44 (9) 3880-4. Journal code: 7703701. ISSN: 0146-0404.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200309
ED Entered STN: 20030827
Last Updated on STN: 20030917
Entered Medline: 20030916
AB PURPOSE: The **optineurin** gene (OPTN) is the second gene besides MYOC in which mutations have been identified to be associated with primary open-angle glaucoma (POAG). In this study, sequence alterations in the OPTN gene associated with POAG in Chinese subjects were investigated. METHODS: All the coding exons of OPTN were screened, including the intron-exon boundaries, for sequence alterations in a Chinese sample of 119 sporadic patients with POAG and 126 unrelated control subjects by **polymerase chain reaction**-conformation-sensitive gel electrophoresis and DNA sequencing. RESULTS: Sixteen sequence changes were identified: 3 had been reported (T34T, M98K, and R545Q) and 13 were novel (T49T, E103D, V148V, P199P, T202T, H486R, IVS6-5T-->C, IVS6-10G-->A, IVS7+24G-->A, IVS8+20G-->A, IVS13+21C-->G, IVS15+10G-->A, and IVS15-48C-->A). Among them, only E103D, H486R, V148V, and IVS13+21C-->G were found exclusively in patients with POAG, whereas P199P, T202T, and IVS8+20G-->A were present only in control subjects. The genotype of IVS7+24G-->A showed a significant association with POAG (P = 0.02, Fisher two-tailed exact test) and with and increased cup-to-disc ratio in these patients (P = 0.005, Mann-Whitney test). CONCLUSIONS: The findings in the current study enrich the evidence on the OPTN gene as a causative gene for POAG and suggest a different mutation pattern of OPTN in Chinese than in whites. The wide spectrum of putative mutations detected in this study suggests that both structural and functional disruptions in OPTN may contribute to the pathogenesis of glaucoma.
TI Different **optineurin** mutation pattern in primary open-angle glaucoma.
AB PURPOSE: The **optineurin** gene (OPTN) is the second gene besides MYOC in which mutations have been identified to be associated with primary open-angle. . . boundaries, for sequence alterations in a Chinese sample of 119 sporadic patients with POAG and 126 unrelated control subjects by **polymerase chain reaction** -conformation-sensitive gel electrophoresis and DNA sequencing. RESULTS: Sixteen sequence changes were identified: 3 had been reported (T34T, M98K, and R545Q) and. . .
CT . . .
DNA Mutational Analysis
Genotype
Glaucoma, Open-Angle: EH, ethnology
*Glaucoma, Open-Angle: GE, genetics
Hong Kong: EP, epidemiology
Middle Aged
*Mutation
Phenotype
Polymerase Chain Reaction
Sequence Analysis, DNA
*Transcription Factor TFIIIA: GE, genetics

L14 ANSWER 4 OF 15 MEDLINE on STN DUPLICATE 2

AN 2003254843 MEDLINE
DN PubMed ID: 12766061
TI Gene expression profile of the human trabecular meshwork: NEIBank sequence tag analysis.
AU Tomarev Stanislav I; Wistow Graeme; Raymond Vincent; Dubois Stephane; Malyukova Irina
CS Laboratory of Molecular and Developmental Biology, National Institutes of Health, Bethesda, Maryland 20892-2730, USA.. tomarevs@nei.nih.gov
SO Investigative ophthalmology & visual science, (2003 Jun) 44 (6) 2588-96. Journal code: 7703701. ISSN: 0146-0404.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS OMIM-602668
EM 200306
ED Entered STN: 20030604
Last Updated on STN: 20030613
Entered Medline: 20030612
AB PURPOSE: To characterize the gene expression pattern in the human trabecular meshwork (TM) and identify candidate genes for glaucoma by expressed sequence tag (EST) analysis as part of the NEIBank project. METHODS: RNA was extracted from dissected human TM and used to construct unamplified, un-normalized cDNA libraries in the pSPORT1 vector. More than 4000 clones were sequenced from the 5' end. Clones were clustered and identified using GRIST software. In addition, the expression patterns of genes encoding olfactomedin-domain proteins were analyzed by RT-**PCR**. RESULTS: After non-mRNA contaminants were removed, 3459 independent TM-expressed clones were obtained. These were grouped in 1888 clusters, potentially representing individual expressed genes. Transcripts for the myocilin gene, a locus for inherited glaucoma, formed the third most abundant cluster in the TM collection, and several other genes implicated in glaucoma (PITX2, CYP1B1, and **optineurin**) were also represented. One abundant TM transcript was from the gene for the angiopoietin-like factor CTD6, which is located at on the long arm of chromosome 1, area 36.2-36.1 in the region of the glaucoma locus GLC3B, whereas other transcripts were from genes close to known glaucoma loci. The TM collection contains cDNAs for genes that are preferentially expressed in the lymphatic endothelium (matrix Gla protein, apolipoprotein D precursor, and selenoprotein P precursor). In addition to EST profiling, RT- **PCR** was used to detect transcripts of the olfactomedin-domain proteins latrotoxin receptor Lec3 and optimedin in the TM. CONCLUSIONS: The TM libraries are a good source of molecular markers for TM and candidate genes for glaucoma. The abundance of myocilin cDNAs corresponds to the critical role of this gene in glaucoma and contrasts with libraries derived from cultured tissue. The expression profile raises the possibility that cells of the TM and Schlemm's canal may be more similar to lymphatic, rather than blood vascular endothelium.
AB . . . were clustered and identified using GRIST software. In addition, the expression patterns of genes encoding olfactomedin-domain proteins were analyzed by RT-**PCR**. RESULTS: After non-mRNA contaminants were removed, 3459 independent TM-expressed clones were obtained. These were grouped in 1888 clusters, potentially representing. . . formed the third most abundant cluster in the TM collection, and several other genes implicated in glaucoma (PITX2, CYP1B1, and **optineurin**) were also represented. One abundant TM transcript was from the gene for the angiopoietin-like factor CTD6, which is located atomic . . in the lymphatic endothelium (matrix Gla protein, apolipoprotein D precursor, and selenoprotein P precursor). In addition to EST profiling, RT- **PCR** was used to detect transcripts of the olfactomedin-domain proteins latrotoxin receptor Lec3 and optimedin in the TM. CONCLUSIONS: The TM. . .
CT . . .
*Gene Expression Profiling

Gene Library
*Glaucoma: GE, genetics
Middle Aged
National Institutes of Health (U.S.)
Ophthalmology
RNA, Messenger: ME, metabolism
Reverse Transcriptase Polymerase Chain Reaction
Sequence Analysis
Sequence Tagged Sites
*Trabecular Meshwork: ME, metabolism
United States

L14 ANSWER 5 OF 15 MEDLINE on STN DUPLICATE 3
AN 2003194953 MEDLINE
DN PubMed ID: 12714628
TI Effects of prostaglandin analogues on human ciliary muscle and trabecular meshwork cells.
AU Zhao Xiujun; Pearson Keri E; Stephan Dietrich A; Russell Paul
CS Laboratory of Mechanisms of Ocular Diseases, National Eye Institute, National Institutes of Health, Bethesda, Maryland, USA.
SO Investigative ophthalmology & visual science, (2003 May) 44 (5) 1945-52. Journal code: 7703701. ISSN: 0146-0404.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200305
ED Entered STN: 20030426
Last Updated on STN: 20030520
Entered Medline: 20030519
AB PURPOSE: To determine the effects of prostaglandin F(2alpha) analogues on gene expression of human ciliary muscle (HCM) and trabecular meshwork (HTM) cells. METHODS: Cultures of HCM and HTM cells were established from five different donors treated for 9 days with 10 microg/mL of either latanoprost (free acid) or prostaglandin F(2alpha) ethanolamide and compared with control cells. The mRNA from the cells of the five individual donors was pooled and analyzed by using gene microarrays. Gene expression changes were confirmed by either real-time **PCR** or relative quantitative **PCR**. RESULTS: Approximately 12 genes showed a twofold or greater change in expression under experimental conditions. Four of these may alter outflow. Aquaporin-1 and versican were downregulated in the HCM, whereas IGF1 and fibroleukin were upregulated in HTM. Expression levels of TNFSF10 and promelanosome-concentrating hormone also increased in the treated HTM cells. The mRNA levels for the prostaglandin FP receptor were downregulated in the ciliary muscle cells. **Optineurin** and alphaB-crystallin levels remained unchanged, but myocilin in the HTM cells was decreased in some samples. CONCLUSIONS: Both analogues changed gene expression similarly in either HCM or HTM cells, but the changes appeared to be cell specific, perhaps indicating that other transcription factors are influential. Outflow of aqueous humor may be increased by the prostaglandin analogues by alterations in the extracellular matrix. Other changes may influence cellular metabolism, such as the increases in IGF1, tumor necrosis factor superfamily-10 and promelanosome-concentrating hormone.
AB . . . the five individual donors was pooled and analyzed by using gene microarrays. Gene expression changes were confirmed by either real-time **PCR** or relative quantitative **PCR**. RESULTS:
Approximately 12 genes showed a twofold or greater change in expression under experimental conditions. Four of these may alter. . . in the treated HTM cells. The mRNA levels for the prostaglandin FP receptor were downregulated in the ciliary muscle cells. **Optineurin** and alphaB-crystallin levels remained unchanged, but myocilin in the HTM cells was decreased in some samples. CONCLUSIONS: Both analogues changed. . .
CT . . .

ME, metabolism
Oligonucleotide Array Sequence Analysis
*Prostaglandins F, Synthetic: PD, pharmacology
RNA: IP, isolation & purification
RNA, Messenger: ME, metabolism
Reverse Transcriptase Polymerase Chain Reaction
*Trabecular Meshwork: DE, drug effects
Trabecular Meshwork: ME, metabolism

L14 ANSWER 6 OF 15 MEDLINE on STN
AN 2003518682 MEDLINE
DN PubMed ID: 14597044
TI Evaluation of **optineurin** sequence variations in 1,048 patients with open-angle glaucoma.
AU Alward Wallace L M; Kwon Young H; Kawase Kazuhide; Craig Jamie E; Hayreh Sohan S; Johnson A Tim; Khanna Cheryl L; Yamamoto Tetsuya; Mackey David A; Roos Benjamin R; Affatigato Louisa M; Sheffield Val C; Stone Edwin M
CS Department of Ophthalmology, University of Iowa Carver College of Medicine, Iowa City, Iowa 52242, USA.
NC EY10564 (NEI)
SO American journal of ophthalmology, (2003 Nov) 136 (5) 904-10. Journal code: 0370500. ISSN: 0002-9394.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 200311
ED Entered STN: 20031105
Last Updated on STN: 20031219
Entered Medline: 20031118
AB PURPOSE: To investigate the association of sequence variations in the **optineurin** (OPTN) gene in patients with open-angle glaucoma. DESIGN: Prospective case control study. METHODS: The OPTN gene was screened for sequence variations using a combination of single-strand conformational polymorphism analysis and automated DNA sequencing. A total of 1,299 subjects (1048 glaucoma patients and 251 controls) were screened for variations in the four portions of the gene that had been previously associated with glaucoma. A subset of these subjects (376 patients and 176 controls) was screened for variations in the entire coding sequence. Twenty-four percent of the patients and 35% of the controls were Japanese, whereas the remainder were predominantly Caucasian. Allele frequencies were compared with the Fisher exact test. RESULTS: The OPTN sequence variations were not significantly associated with any form of high-tension open-angle glaucoma. One proband with familial normal-tension glaucoma was found to harbor the previously reported Glu50Lys variation. Another previously reported change, Met98Lys, was associated with normal-tension glaucoma in Japanese but not in Caucasian patients. CONCLUSIONS: This study provides some additional evidence for the association of the Glu50Lys OPTN sequence variation with familial normal tension glaucoma. However, because familial normal-tension glaucoma is so rare, this change seems to be responsible for less than 0.1% of all open-angle glaucoma. The Arg545Gln variation is likely to be a nondisease-causing polymorphism. The Met98Lys change may be associated with a fraction of normal-tension glaucoma in patients of Japanese ethnicity.
TI Evaluation of **optineurin** sequence variations in 1,048 patients with open-angle glaucoma.
AB PURPOSE: To investigate the association of sequence variations in the **optineurin** (OPTN) gene in patients with open-angle glaucoma. DESIGN: Prospective case control study. METHODS: The OPTN gene was screened for sequence. . .
CT . . .
Studies
DNA Primers: CH, chemistry

*Eye Proteins: GE, genetics
*Glaucoma, Open-Angle: GE, genetics
Middle Aged
*Nerve Tissue Proteins: GE, genetics
Polymerase Chain Reaction
Polymorphism, Single-Stranded Conformational
Prospective Studies
Sequence Analysis, DNA
CN 0 (DNA Primers); 0 (Eye Proteins); 0 (Nerve Tissue Proteins); 0 (**optineurin**)

L14 ANSWER 7 OF 15 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
AN 2003493555 EMBASE
TI The M98K variant of the **OPTINEURIN** (OPTN) gene modifies initial intraocular pressure in patients with primary open angle glaucoma.
AU Melki R.; Belmouden A.; Akhayat O.; Brezin A.; Garchon H.-J.
CS Dr. H.-J. Garchon, INSERM U580, Hopital Necker, 161 rue de Sevres, 75743 Paris Cedex 15, France. garchon@necker.fr
SO Journal of Medical Genetics, (2003) 40/11 (842-844).
Refs: 13
ISSN: 0022-2593 CODEN: JMDGAE
CY United Kingdom
DT Journal; Article
FS 012 Ophthalmology
022 Human Genetics
LA English
TI The M98K variant of the **OPTINEURIN** (OPTN) gene modifies initial intraocular pressure in patients with primary open angle glaucoma.
CT Medical Descriptors:
*open angle glaucoma: ET, etiology
*intraocular pressure
risk factor
informed consent
genotype
restriction fragment length polymorphism
polymerase chain reaction
exon
gene mutation
human
major clinical study
controlled study
article
nucleotide sequence
priority journal
***optineurin: EC, endogenous compound**
*protein: EC, endogenous compound
myocillin: EC, endogenous compound
unclassified drug

L14 ANSWER 8 OF 15 MEDLINE on STN DUPLICATE 4
AN 2003262740 MEDLINE
DN PubMed ID: 12789137
TI The role of TIGR and OPTN in Finnish glaucoma families: a clinical and molecular genetic study.
AU Forsman Eva; Lemmela Susanna; Varilo Teppo; Kristo Paula; Forsius Henrik; Sankila Eeva-Marja; Jarvela Irma
CS Population Genetics Unit, Folkhalsan Institute of Genetics, Helsinki, Finland.
SO Molecular vision [electronic resource], (2003 May 30) 9 217-22.
Journal code: 9605351. ISSN: 1090-0535.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
EM 200306
ED Entered STN: 20030606
Last Updated on STN: 20030624
Entered Medline: 20030623
AB PURPOSE: The aim of the present study was to analyze the role of the two primary open angle glaucoma (POAG) genes, trabecular meshwork-induced glucocorticoid response (TIGR/MYOC) and **optineurin** (OPTN), in Finnish glaucoma families originating from southern coast of Finland. METHODS: In total, 136 patients were examined to determine their ophthalmological status. Genealogical studies were performed using church records. Direct **PCR**-sequencing of the coding regions of the TIGR and OPTN genes was performed in 11 subjects. RESULTS: Inheritance resembling autosomal dominant mode was detected in eight families with open-angle glaucoma. Glaucoma was diagnosed in 53 subjects, of them 44 had POAG, 7 had exfoliative glaucoma (EG), and 2 had other types of glaucoma. Of the first degree relatives, 22 out of 79 (28%) were glaucoma suspects. No mutations in these families were identified. Instead, two polymorphisms in the TIGR gene and three polymorphisms in the OPTN gene, in which one was novel, were found in three phenotypes: POAG, exfoliative glaucoma, and exfoliation syndrome. CONCLUSIONS: Our results give evidence that novel, unidentified genes will underlie POAG and exfoliation syndrome in the Finnish population.
AB . . . was to analyze the role of the two primary open angle glaucoma (POAG) genes, trabecular meshwork-induced glucocorticoid response (TIGR/MYOC) and **optineurin** (OPTN), in Finnish glaucoma families originating from southern coast of Finland. METHODS: In total, 136 patients were examined to determine their ophthalmological status. Genealogical studies were performed using church records. Direct **PCR**-sequencing of the coding regions of the TIGR and OPTN genes was performed in 11 subjects. RESULTS: Inheritance resembling autosomal dominant. . .
CT . . .
*Glycoproteins: GE, genetics
Intraocular Pressure
Middle Aged
Molecular Biology
Mutation
*Nerve Tissue Proteins: GE, genetics
Ocular Hypertension: GE, genetics
Pedigree
Polymerase Chain Reaction
Polymorphism (Genetics): GE, genetics
CN 0 (Eye Proteins); 0 (Glycoproteins); 0 (Nerve Tissue Proteins); 0 (**optineurin**); 0 (trabecular meshwork-induced glucocorticoid response protein)

L14 ANSWER 9 OF 15 MEDLINE on STN DUPLICATE 5
AN 2003132783 MEDLINE
DN PubMed ID: 12646749
TI **Optineurin** gene expression level in human trabecular meshwork does not change in response to pressure elevation.
AU Kamphuis Willem; Schneemann Andrea
CS Netherlands Ophthalmic Research Institute-KNAW, Glaucoma Research Group, Amsterdam, The Netherlands.. w.kamphuis@ioi.knaw.nl
SO Ophthalmic research, (2003 Mar-Apr) 35 (2) 93-6.
Journal code: 0267442. ISSN: 0030-3747.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200305
ED Entered STN: 20030321
Last Updated on STN: 20030528

Entered Medline: 20030527

AB Mutations in the gene **optineurin** (OPTN) have been associated with primary-open angle glaucoma. Here we present a study on the level of OPTN gene expression in the human trabecular meshwork in response to increased perfusion pressure in the anterior chamber perfusion model of the human eye. Perfusion pressure was raised from 10 to 30 mm Hg for periods ranging between 1 and 24 h. OPTN transcript levels in the trabecular meshwork were determined using real-time quantitative **polymerase chain reaction**. The results show no statistically significant alteration of the OPTN transcript level after raising the pressure. Moreover, no changes were detected in the transcript levels of the 3 known OPTN isoforms. This result shows that enhanced pressure levels do not lead to rapid changes in gene expression levels of OPTN in human trabecular meshwork. This suggests that alterations in OPTN gene expression are not involved in the mechanisms regulating aqueous humor outflow after an increase in intraocular eye pressure.

TI **Optineurin** gene expression level in human trabecular meshwork does not change in response to pressure elevation.

AB Mutations in the gene **optineurin** (OPTN) have been associated with primary-open angle glaucoma. Here we present a study on the level of OPTN gene expression. . . for periods ranging between 1 and 24 h. OPTN transcript levels in the trabecular meshwork were determined using real-time quantitative **polymerase chain reaction**. The results show no statistically significant alteration of the OPTN transcript level after raising the pressure. Moreover, no changes were. . .

CT . . .

Eye Proteins: GE, genetics
Gene Expression
*Intraocular Pressure: PH, physiology
*Nerve Tissue Proteins: BI, biosynthesis
Nerve Tissue Proteins: GE, genetics
Polymerase Chain Reaction: MT, methods
RNA, Messenger: BI, biosynthesis
*Trabecular Meshwork: ME, metabolism
Trabecular Meshwork: PH, physiology

CN 0 (Eye Proteins); 0 (Nerve Tissue Proteins); 0 (RNA, Messenger); 0 (**optineurin**)

L14 ANSWER 10 OF 15 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:543728 BIOSIS
DN PREV200300539231
TI GENE EXPRESSION PROFILE OF THE HUMAN TRABECULAR MESHWORK.
AU Tomarev, S. I. [Reprint Author]; Wistow, G.; Raymond, V.; Dubois, S.; Malyukova, I. [Reprint Author]
CS NEI/NIH, Bethesda, MD, USA
SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 3166. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 19 Nov 2003
Last Updated on STN: 19 Nov 2003

AB Purpose: To characterize gene expression pattern in the human trabecular meshwork (TM) and identify candidate genes for glaucoma by expressed sequence tag (EST) analysis. Methods: RNA was extracted from dissected human TM and used to construct unamplified, un-normalized cDNA libraries in the pSPORT1 vector. Over 4000 clones were sequenced from their 5'end. Clones were clustered and identified using the GRIST software. In

addition, the expression patterns of genes encoding olfactomedin-domain proteins were analyzed by RT-**PCR**. Results: After removing non-mRNA contaminants, 3459 independent TM-expressed clones were obtained. These grouped into 1888 clusters, potentially representing individual expressed genes. Transcripts for the myocilin gene, a locus for inherited glaucoma, formed the third most abundant cluster in the TM collection, while several other genes implicated in glaucoma (PITX2, CYP1B1 and **optineurin**) were also represented. One abundant TM transcript was from the gene for the angiopoietin-like factor CTD6, which is located at chromosome 1p36.2-p36.1 in the region of the glaucoma locus GLC3B, while other transcripts were from genes close to known glaucoma loci. The TM collection contained cDNAs for genes that are preferentially expressed in the lymphatic endothelium (matrix Gla protein, apolipoprotein D precursor, selenoprotein P precursor). In addition to EST profiling, RT- **PCR** was used to detect transcripts of the olfactomedin-domain proteins latrotoxin receptor Lec3 and optimedin in the TM. Conclusions: The TM libraries were a good source of molecular markers for TM and candidate genes for glaucoma. The abundance of myocilin cDNAs corresponded to the critical role of this gene in glaucoma and contrasted with libraries derived from cultured tissue. Our expression profile analysis raises the possibility that cells of the TM and Schlemm's canal may be more similar to lymphatic, rather than blood vascular endothelium.

AB. . . clustered and identified using the GRIST software. In addition, the expression patterns of genes encoding olfactomedin-domain proteins were analyzed by RT-**PCR**. Results: After removing non-mRNA contaminants, 3459 independent TM-expressed clones were obtained. These grouped into 1888 clusters, potentially representing individual expressed. . . formed the third most abundant cluster in the TM collection, while several other genes implicated in glaucoma (PITX2, CYP1B1 and **optineurin**) were also represented. One abundant TM transcript was from the gene for the angiopoietin-like factor CTD6, which is located atomic . . expressed in the lymphatic endothelium (matrix Gla protein, apolipoprotein D precursor, selenoprotein P precursor). In addition to EST profiling, RT- **PCR** was used to detect transcripts of the olfactomedin-domain proteins latrotoxin receptor Lec3 and optimedin in the TM. Conclusions: The TM. . .

IT Methods & Equipment
RT-**PCR** [reverse transcriptase-**polymerase chain reaction**]: genetic techniques, laboratory techniques; expressed sequence tag analysis: laboratory techniques

IT Miscellaneous Descriptors
gene expression profile

GEN CYP1B1 gene; PITX2 gene; myocilin gene; **optineurin** gene

L14 ANSWER 11 OF 15 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:529130 BIOSIS
DN PREV200300524884
TI EXPRESSION OF **OPTINEURIN** IN HUMAN ANTERIOR SEGMENT ORGAN CULTURES SUBJECTED TO GLAUCOMATOUS INSULTS.
AU Vittitow, J. L. [Reprint Author]; Wei, X. [Reprint Author]; Borras, T. [Reprint Author]
CS Department of Ophthalmology, The University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 1163. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003
AB Purpose: Mutations in **optineurin** (OPTN) have been linked to

families with primary open-angle glaucoma. Here we determined the expression profile for this novel gene in the trabecular meshwork (TM) under conditions mimicking physiological pressure. We studied the OPTN expression in response to three factors known to be associated with the development of glaucoma: elevated intraocular pressure (IOP), tumor necrosis factor-alpha (TNFalpha) and dexamethasone (DEX). Methods: Anterior segment pairs from non-glaucomatous post-mortem human eyes were perfused for 24 h at constant flow of 3 mul/min with serum-free tissue culture medium. For elevated pressure experiments, the flow in one eye was raised to obtain a DELTAP of 35 mmHg for either 6 h, 2, 4 or 7 days. The flow of the contralateral, control eye was maintained at 3 mul/min. For drug treatments, both eyes were maintained at their basal flow rate. One eye of each pair was perfused with medium containing either 25 ng/ml TNFalpha for 3 days or 0.1 muM DEX for 7 days. At the end of each experiment, TM cDNA libraries were constructed and expression of OPTN and 18S RNA of the treated eyes versus that of their paired controls was determined by relative quantative RT-**PCR**. Results: OPTN gene expression was up-regulated after 6 h of high IOP (8.2 +- 3.9%, P = 0.07) which increased and became significant after 2 days (9.6% +- 4.2%, P = 0.03), 4 days (40.2% +- 4.5%, P = 0.00001) and 7 days (55.6% +- 3.3%, P = 0.0002) (n = 9 for each time point). OPTN expression was also induced 2.3 +- 0.05-fold (P = 0.008) in TMs treated with TNFalpha (n = 6) and 2.6 +- 0.12-fold (P = 0.0002) in those treated with DEX (n = 9). Conclusions: These findings demonstrate that OPTN belongs to the trabecular meshwork transcriptome that responds to insults involved in glaucomatous occurrences and support the notion that OPTN may be part of a general protective mechanism present in the cells of the outflow pathway.

TI EXPRESSION OF **OPTINEURIN** IN HUMAN ANTERIOR SEGMENT ORGAN CULTURES SUBJECTED TO GLAUCOMATOUS INSULTS.

AB Purpose: Mutations in **optineurin** (OPTN) have been linked to families with primary open-angle glaucoma. Here we determined the expression profile for this novel gene. . . of OPTN and 18S RNA of the treated eyes versus that of their paired controls was determined by relative quantative RT-**PCR**. Results: OPTN gene expression was up-regulated after 6 h of high IOP (8.2 +- 3.9%, P = 0.07) which increased. . .

IT . . .
segment: sensory system; trabecular meshwork: sensory system

IT Diseases
glaucoma: eye disease
Glaucoma (MeSH)

IT Chemicals & Biochemicals
cDNA library; dexamethasone; **optineurin**: expression; tumor necrosis factor-alpha [TNF-alpha]

GEN OPTN gene [**optineurin** gene]

L14 ANSWER 12 OF 15 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:529108 BIOSIS
DN PREV200300524870
TI EFFECTS OF PROSTAGLANDIN ANALOGUES ON THE FP RECEPTOR AND GENES ASSOCIATED WITH GLAUCOMA.
AU Zhao, X. [Reprint Author]; Russell, P. [Reprint Author]
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SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 1149. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DT Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 12 Nov 2003

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AB Purpose: To determine the effects of prostaglandin analogues on the FP receptor and genes associated with glaucoma in human ciliary muscle (HCM) and trabecular meshwork (HTM) cells. Methods: Cultures of HCM and HTM cells were established from five different donors, treated for nine days with 10 mug/ml of either latanoprost free acid or prostaglandin F2alpha ethanolamide and compared to control cells. The mRNA from the cells of the five individual donors was extracted and purified. Gene expression changes were performed by either Real-Time **PCR** or relative quantitative **PCR**. Results: The mRNA levels for the prostaglandin FP receptor were down regulated in the human ciliary muscle cells when treated with either of the two prostaglandin analogues, while there were no changes in HTM with such treatment. **Optineurin** and alphaB-crystallin levels remained unchanged, but myocilin in the HTM cells was decreased in some samples. Conclusions: Both analogues changed gene expression similarly in either HCM or HTM cells. Down-regulated prostaglandin FP receptor in HCM when treated with prostaglandin analogues indicated that reduction of the receptor might have profound impact on long-term efficacy of such drugs. Prostaglandin analogues showed little impact on the gene associated with glaucoma in either HCM or HTM cells.

AB. . . from the cells of the five individual donors was extracted and purified. Gene expression changes were performed by either Real-Time **PCR** or relative quantitative **PCR**. Results: The mRNA levels for the prostaglandin FP receptor were down regulated in the human ciliary muscle cells when treated with either of the two prostaglandin analogues, while there were no changes in HTM with such treatment. **Optineurin** and alphaB-crystallin levels remained unchanged, but myocilin in the HTM cells was decreased in some samples. Conclusions: Both analogues changed. . .

IT . . .

IT Diseases
glaucoma: eye disease
Glaucoma (MeSH)

IT Chemicals & Biochemicals
FP receptor; alpha-B crystallin; latanoprost free acid: antiglaucoma-drug, ophthalmic-drug; myocilin; **optineurin**; prostaglandin F-2-alpha ethanolamide: ophthalmic-drug; prostaglandin FP receptor mRNA [prostaglandin FP receptor messenger RNA]: expression

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TI EXPRESSION OF PORCINE MYOCILIN AND **OPTINEURIN** IN TRABECULAR MESHWORK CELLS AND ASTROCYTES FROM OPTIC NERVE HEAD.

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SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 1115. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)

LA English

ED Entered STN: 5 Nov 2003
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AB Purpose: Recently, **optineurin** (OPTN), a new gene responsible for primary open-angle glaucoma and normal tension glaucoma was identified (Sarfarazi et al. Science 2002). To compare the expression of OPTN with myocilin (MYOC) we determined the complete sequence of porcine OPTN cDNA and performed quantitative-**PCR** analysis on two porcine primary

cells, trabecular meshwork cells (TMC) and astrocytes, cultured under various stimuli and stresses, which mimic the glaucoma cellular conditions. Methods: Coding region of porcine OPTN cDNA was amplified by RT-**PCR** from porcine TMC total RNA using primers designed from conserved sequence between human, mouse, and rat. The lacking 5' and 3' cDNA ends were amplified by 5' and 3' RACE method respectively. Total RNA was isolated from cultured cells treated with dexamethasone (500nM, for 2weeks), hydrostatic pressure (+30mmHg, 72h) or hypoxia (7% O2, 72h). The expression level of the OPTN and MYOC in TMC and astrocytes were analyzed by real-time quantitative **PCR** (GeneAmp5700, PE Biosystems, Inc.). Total RNA used for quantitation was treated with DNase prier to measurement. Results: Porcine OPTN protein was composed of 574 amino acids, which was 84% identical with that of human OPTN protein. Treatment with dexamethasone increased MYOC expression by 8.2-fold and 5.5-fold in TMC and astrocytes respectively, while OPTN was suppressed to 48% in astrocytes and 68% in TMC. Incubation under hypoxia showed significant decrease for MYOC in both cells, while OPTN transcript was not affected. Hydrostatic pressure did not affect both genes in both cells. Conclusions: Nucleotide sequence of full-length porcine OPTN cDNA was determined and showed high degree of homology with human. OPTN expression was compared with MYOC under stimuli or stress in two porcine primary cells. Expression of OPTN was suppressed by dexamethasone but no effect was observed under hypoxia or hydrostatic pressure.

TI EXPRESSION OF PORCINE MYOCILIN AND **OPTINEURIN** IN TRABECULAR MESHWORK CELLS AND ASTROCYTES FROM OPTIC NERVE HEAD.

AB Purpose: Recently, **optineurin** (OPTN), a new gene responsible for primary open-angle glaucoma and normal tension glaucoma was identified (Sarfarazi et al. Science 2002).. . . To compare the expression of OPTN with myocilin (MYOC) we determined the complete sequence of porcine OPTN cDNA and performed quantitative-**PCR** analysis on two porcine primary cells, trabecular meshwork cells (TMC) and astrocytes, cultured under various stimuli and stresses, which mimic the glaucoma cellular conditions. Methods: Coding region of porcine OPTN cDNA was amplified by RT-**PCR** from porcine TMC total RNA using primers designed from conserved sequence between human, mouse, and rat. The lacking 5' and. . . (7% O2, 72h). The expression level of the OPTN and MYOC in TMC and astrocytes were analyzed by real-time quantitative **PCR** (GeneAmp5700, PE Biosystems, Inc.). Total RNA used for quantitation was treated with DNase prier to measurement. Results: Porcine OPTN protein. . .

IT . . .
head: nervous system; trabecular meshwork cell: sensory system

IT Diseases
glaucoma: eye disease
Glaucoma (MeSH)

IT Chemicals & Biochemicals
dexamethasone: glucocorticoid-drug; **optineurin** cDNA; total RNA

GEN porcine MYOC gene [porcine myocilin gene] (Suidae): expression; porcine OPTN gene [porcine **optineurin** gene] (Suidae): expression

L14 ANSWER 14 OF 15 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2003:518129 BIOSIS
DN PREV200300512386
TI ANALYSIS OF **OPTINEURIN** - RAB8 PROTEIN INTERACTION UISNG QUARTZ - CRYSTAL MICROBALANCE (QCM).
AU Iwata, T. [Reprint Author]; Sanuki, N. [Reprint Author]; Mashima, Y.; Tanaka, Y. [Reprint Author]
CS Natl Center for Sensory Organs, National Tokyo Medical Center, Tokyo, Japan
SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 1114. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association

for Research in Vision and Ophthalmology.
DT Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 5 Nov 2003
Last Updated on STN: 5 Nov 2003
AB Purpose: Recently Sarfarazi et al. (Science 2002) identified a new gene **optineurin** (OPTN) responsible for primary open-angle glaucoma and normal tension glaucoma. This protein was previously characterized to interact with several proteins including RAB8. To further characterize the effect of mutation to OPTN-RAB8 protein interaction, Quartz-Crystal Microbalance (QCM), a new method to analyze protein-protein interaction was applied. Methods: Human OPTN was amplified by RT-**PCR** from human kidney total RNA and cloned into N-terminal His-tag bacterial expression vector pTrcHis (Invitrogen). Mutations 458G>A, 691_692insAG, 1944G>A, and SNP 603T>A were introduced with Quick Change Multi Site-Directed Mutagenesis Kit (Stratagene). Bacteria TOP10 was transformed with each OPTN construct and incubated for 6h under 1mM IPTG. OPTN was purified by affinity (HiTrap Chelating HP) and gel filtration (Superdex-75 HR 10/30) chromatography with HPLC AKTA Explorer (Amersham Biosciences). RAB8 was amplified by RT-**PCR** from brain total RNA and cloned for expression. Purification was performed by the same procedure. Quartz-Crystal Microbalance (AffinixQ, Initium) was used to measure protein-protein interaction of two purified protein in PBS solution containing blocking reagent for AffinixQ. Thirty to three hundred nanograms of purified RAB8 were attached to QCM chip. Various amount of OPTN dissolved in 8ul of 20mM phosphate buffer (pH7.6) was injected into 8ml PBS solution in QCM interaction chamber for interaction measurement. Results: All the constructs with mutation had significant reduction of protein expression compared with wild type. Mutant OPTN 458G>A showed weak binding to the affinity column presumably due to the conformational change in protein structure. OPTN with mutation had significantly weak affinity to purified RAB8 protein. Detail numbers will be presented at the meeting. Conclusions: QCM, a new method to analyze protein-protein interaction was applied to characterize OPTN-RAB8 protein interaction. Mutations and polymorphism reported by Sarfarazi et al. (Science 2002) were introduced into wild type OPTN cDNA. These OPTN constructs were then expressed and purified for one to one interaction with purified RAB8 protein. Interaction with RAB8 was significantly affected by several mutations.
TI ANALYSIS OF **OPTINEURIN** - RAB8 PROTEIN INTERACTION UISNG QUARTZ - CRYSTAL MICROBALANCE (QCM).
AB Purpose: Recently Sarfarazi et al. (Science 2002) identified a new gene **optineurin** (OPTN) responsible for primary open-angle glaucoma and normal tension glaucoma. This protein was previously characterized to interact with several proteins. . . protein interaction, Quartz-Crystal Microbalance (QCM), a new method to analyze protein-protein interaction was applied. Methods: Human OPTN was amplified by RT-**PCR** from human kidney total RNA and cloned into N-terminal His-tag bacterial expression vector pTrcHis (Invitrogen). Mutations 458G>A, 691_692insAG, 1944G>A, and. . . (HiTrap Chelating HP) and gel filtration (Superdex-75 HR 10/30) chromatography with HPLC AKTA Explorer (Amersham Biosciences). RAB8 was amplified by RT-**PCR** from brain total RNA and cloned for expression. Purification was performed by the same procedure. Quartz-Crystal Microbalance (AffinixQ, Initium) was. . .
IT Methods & Equipment
quartz-crystal microbalance: laboratory techniques
IT Miscellaneous Descriptors
optineurin-rab8 protein interaction
GEN human OPTN gene [human **optineurin** gene] (Hominidae): expression, mutation

L14 ANSWER 15 OF 15 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

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DN PREV200300512383
TI **OPTINEURIN** GENE POLYMORPHISMS IN JAPANESE GLAUCOMA PATIENTS AND NORMAL INDIVIDUALS.
AU Umeda, T. [Reprint Author]; Matsuo, T. [Reprint Author]; Tanabe, Y. [Reprint Author]; Nagayama, M. [Reprint Author]; Tamura, N. [Reprint Author]; Ohtsuki, H. [Reprint Author]
CS Ophthalmology, Okayama Univ Grad Sch Med Dent, Okayama, Japan
SO ARVO Annual Meeting Abstract Search and Program Planner, (2003) Vol. 2003, pp. Abstract No. 1111. cd-rom.
Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology. Fort Lauderdale, FL, USA. May 04-08, 2003. Association for Research in Vision and Ophthalmology.
DT Conference; (Meeting)
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Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 5 Nov 2003
Last Updated on STN: 5 Nov 2003
AB Purpose: **Optineurin** mutations have been recently identified as responsible for the GLC1E locus of open angle glaucoma (Science2002;295:1077-9). This study aimed at detecting mutations and polymorphisms of **optineurin** gene (OPTN) in Japanese patients with various types of glaucoma as well as in normal Japanese individuals. Methods: The exons 4, 5, 6, and 16 of OPTN in 149 patients with various types of glaucoma and 43 normal individuals were amplified by **polymerase chain reaction** from genomic DNA of peripheral blood leukocytes and then submitted to direct sequencing. Included in the study were 67 patients with primary open angle glaucoma (POAG), 27 with normal tension glaucoma (NTG), 21 with secondary glaucoma (SG), 8 with capsular glaucoma (CapG), 9 with congenital glaucoma (ConG), 12 with primary angle-closure glaucoma (PACG), 4 with ocular hypertension (OH), and one with Chandler syndrome. Results: The reported heterozygous mutations, 458G>A(Glu50Lys) in exon 4 and 691_692insAG in exon 6 were not found in any glaucoma patients or normal individuals. The reported 603T>A(Met98Lys) in exon 5 was found in 9(13.4%) POAG, 2(7.4%) NTG, 3(14.2%) SG, one(12.5%) CapG, one(8.3%) PACG patients, and 4(9.3%) normal individuals. The reported 1944G>A(Arg545Gln) in exon 16 was found in 3(4.4%) POAG, one(3.7%) NTG, 2(9.5%) SG, 2(25.0%) CapG, one(8.3%) PACG patients, and 3(6.9%) normal individuals. In addition, a heterozygous change, 412G>A(Thr34Thr) in exon 4 was found in 18(26.8%) POAG, 4(14.8%) NTG, 4(19.0%) SG, 2(25.0%) CapG, 3(33.3%) ConG, 3(25.0%) PACG patients, and 6(13.9%) normal individuals. Another heterozygous change, 457C>T(Thr49Thr) in exon 4 was found only in 3(4.4%) POAG patients. Conclusions: The reported OPTN mutations were found as polymorphisms both in Japanese glaucoma patients and normal individuals. This population may harbor different types of OPTN polymorphisms as compared to the initial report.
TI **OPTINEURIN** GENE POLYMORPHISMS IN JAPANESE GLAUCOMA PATIENTS AND NORMAL INDIVIDUALS.
AB Purpose: **Optineurin** mutations have been recently identified as responsible for the GLC1E locus of open angle glaucoma (Science2002;295:1077-9). This study aimed at detecting mutations and polymorphisms of **optineurin** gene (OPTN) in Japanese patients with various types of glaucoma as well as in normal Japanese individuals. Methods: The exons. . . 6, and 16 of OPTN in 149 patients with various types of glaucoma and 43 normal individuals were amplified by **polymerase chain reaction** from genomic DNA of peripheral blood leukocytes and then submitted to direct sequencing. Included in the study were 67 patients. . .
GEN human OPTN gene [human **optineurin** gene] (Hominidae): exons, mutation, polymorphism